

In the Claims

Please cancel claim 57

Please amend claim 58 as follows.

Please add the following new claims.

Claim Listing

Claim 1-57 (Canceled)

58. (Currently Amended) A method of identifying a nucleotide sequence comprising comparing a target sequence to a sequence stored in computer readable medium having recorded thereon at least 100 nucleotide sequences including sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof, and identifying said target sequence as being present in the computer readable medium.

59. (New) A method for identifying a nucleic acid sequence comprising:

- a) providing a target nucleotide sequence;
- b) comparing said target nucleotide sequence to one or more nucleotide sequences stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof; and
- c) identifying said target nucleotide sequence as having significant sequence identity to said one or more nucleotide sequences stored in a computer readable medium.

60. (New) The method according to claim 59, wherein said target sequence shares between 100% and 90% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.
61. (New) The method according to claim 60, wherein said target sequence shares between 100% and 95% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.
62. (New) The method according to claim 61 wherein said target sequence shares between 100% and 98% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.
63. (New) The method according to claim 62 wherein said target sequence shares between 100% and 99% sequence identity with one or more of said nucleotide sequences stored on a computer readable medium.
64. (New) The method according to claim 59, wherein said target sequence is identified as homologous to an open reading frame (ORF) within said nucleotide sequence stored on a computer readable medium.
65. (New) The method of claim 59, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.
66. (New) The method of claim 59, wherein said target sequence is identified as homologous to a sequence encoding an *Emericella nidulans* protein or fragment thereof within said one or more nucleotide sequences stored on a computer readable medium.

67. (New) A method of detecting a nucleotide sequence comprising:
- a) providing a target nucleotide sequence;
 - b) comparing said target nucleotide sequence to a nucleotide sequence stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof; and
 - c) identifying said target sequence as homologous to said nucleotide sequence.
68. (New) The method according to claim 67, wherein said target sequence is homologous to an open reading frame (ORF) within said nucleotide sequence.
69. (New) The method of claim 67, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.
70. (New) The method of claim 67, wherein said target sequence is identified according to degree of homology to said nucleotide sequence stored in a computer readable medium.
71. (New) A method of ranking a target nucleotide sequence by homology to a nucleotide sequence of *E. nidulans* comprising:
- a) providing a target nucleotide sequence;
 - b) comparing said target nucleotide sequence to a nucleotide sequence stored in a computer readable medium having recorded thereon at least 100 nucleotide sequences

including sequences selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof; and

- c) ranking said target sequence by degree of homology to said nucleotide sequence of *E. nidulans*.
72. (New) The method of claim 71, wherein said target sequence is a nucleotide sequence of between about 30 and about 300 nucleotide residues in length.